

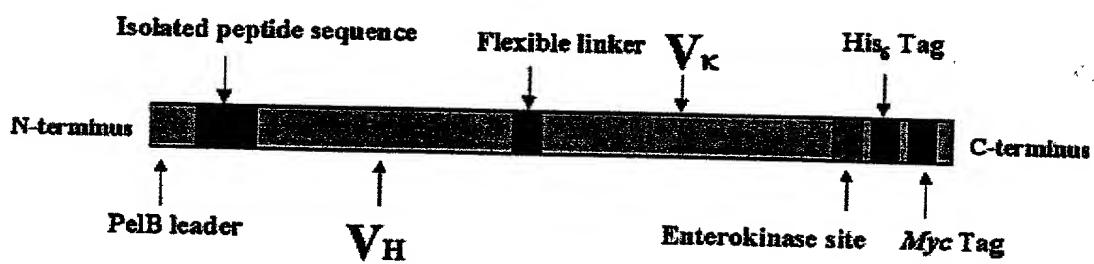
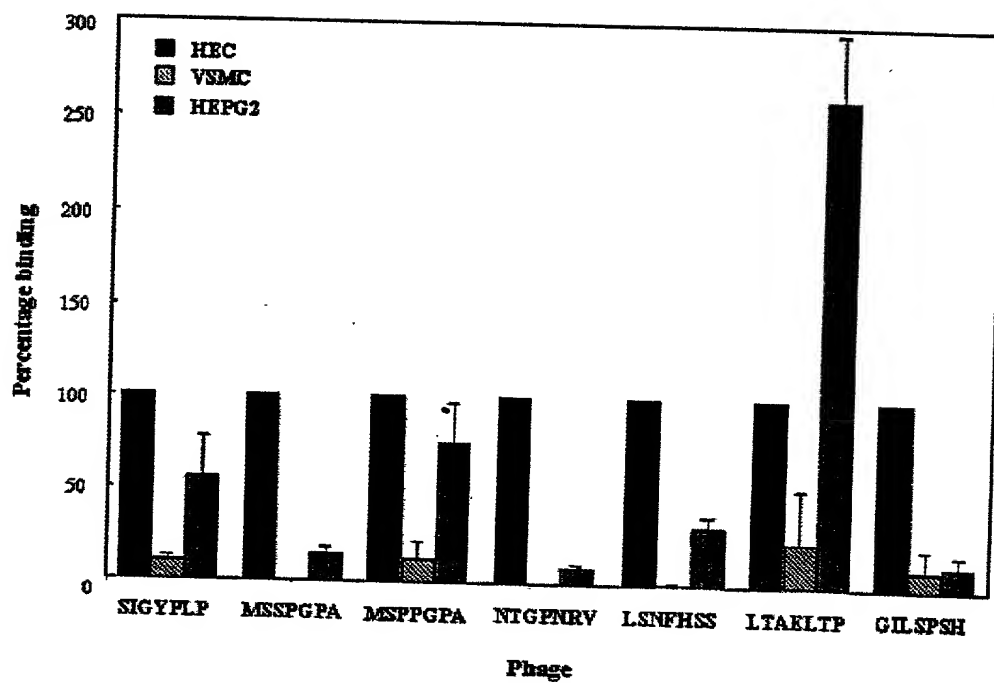
FIGURE 1**FIGURE 2**

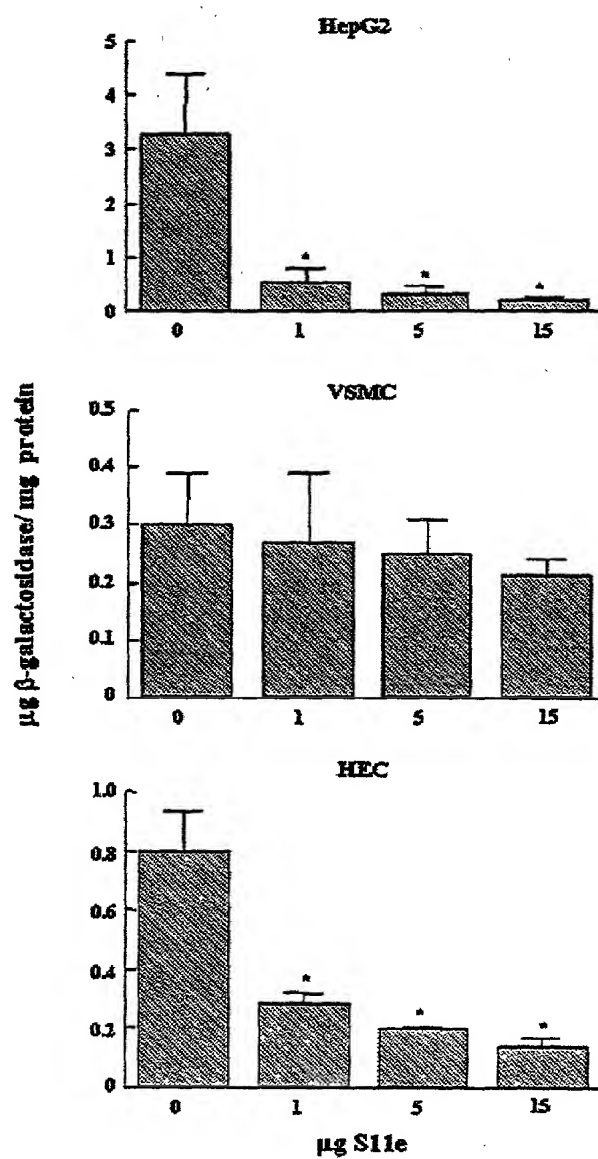
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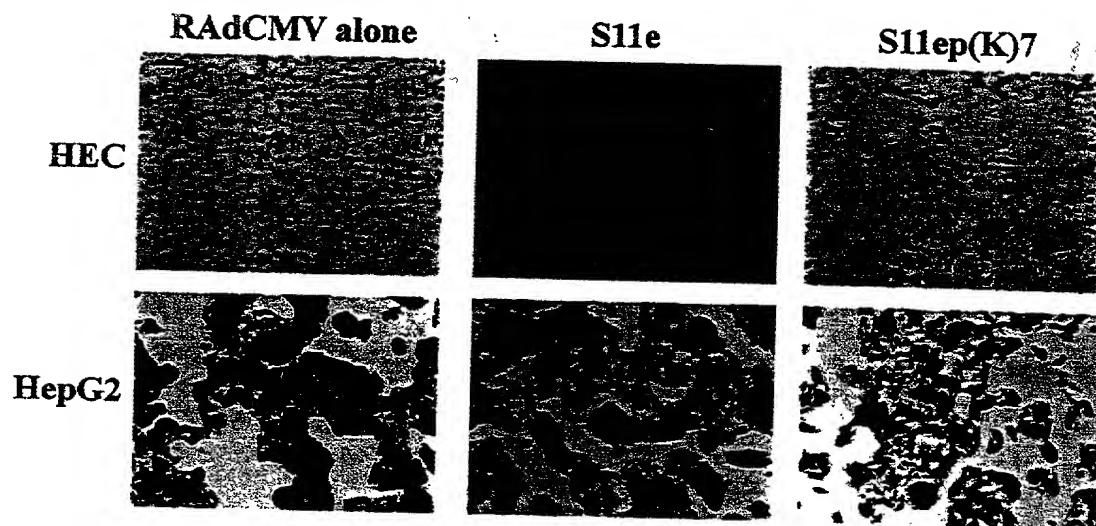
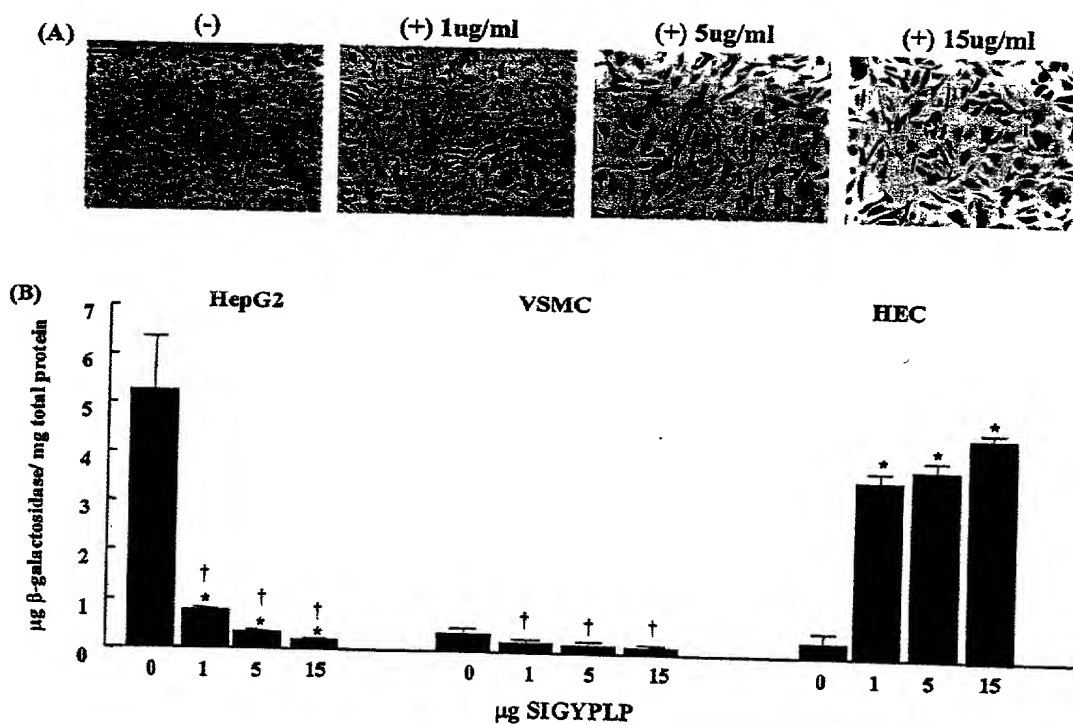
FIGURE 4**FIGURE 5**

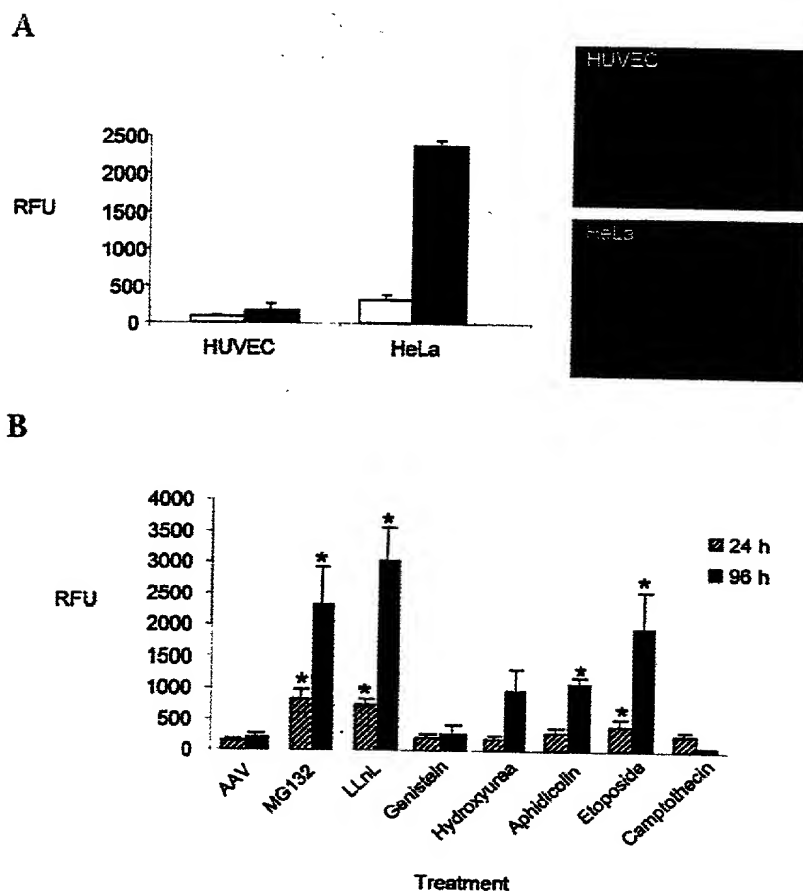
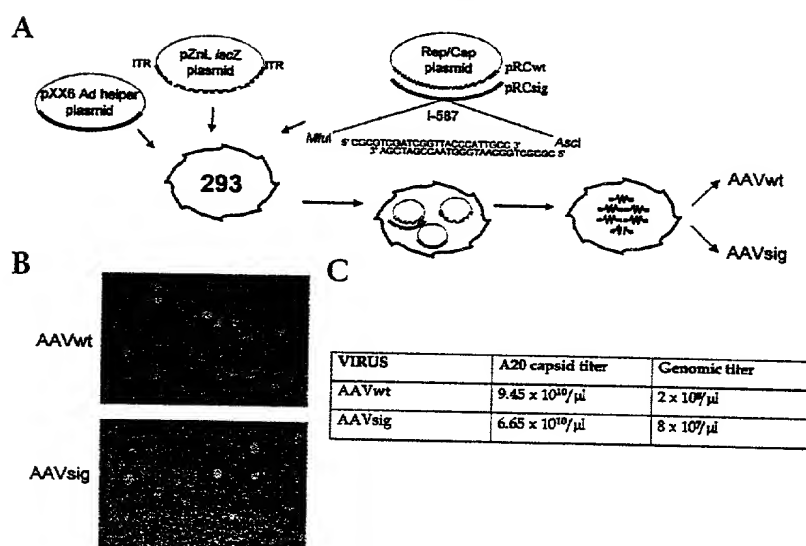
FIGURE 6**FIGURE 7**

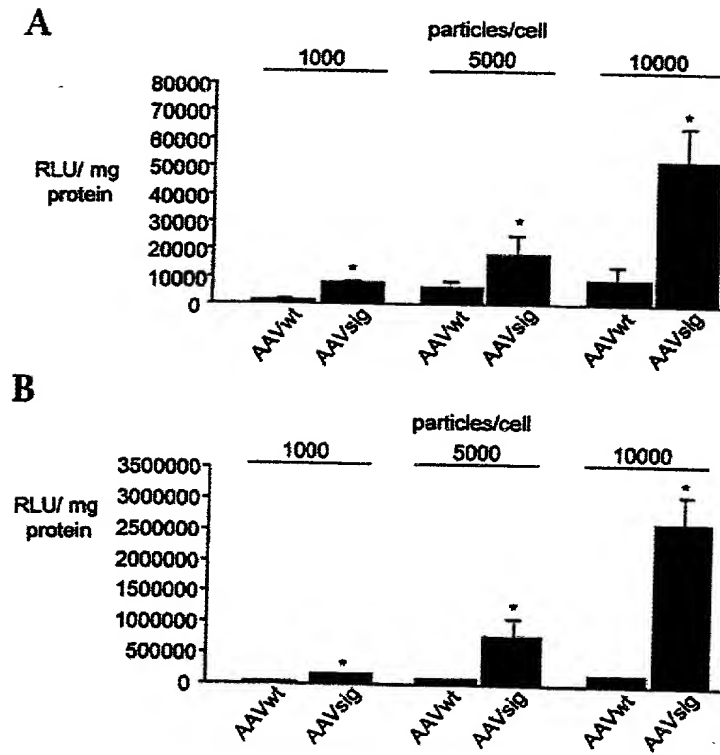
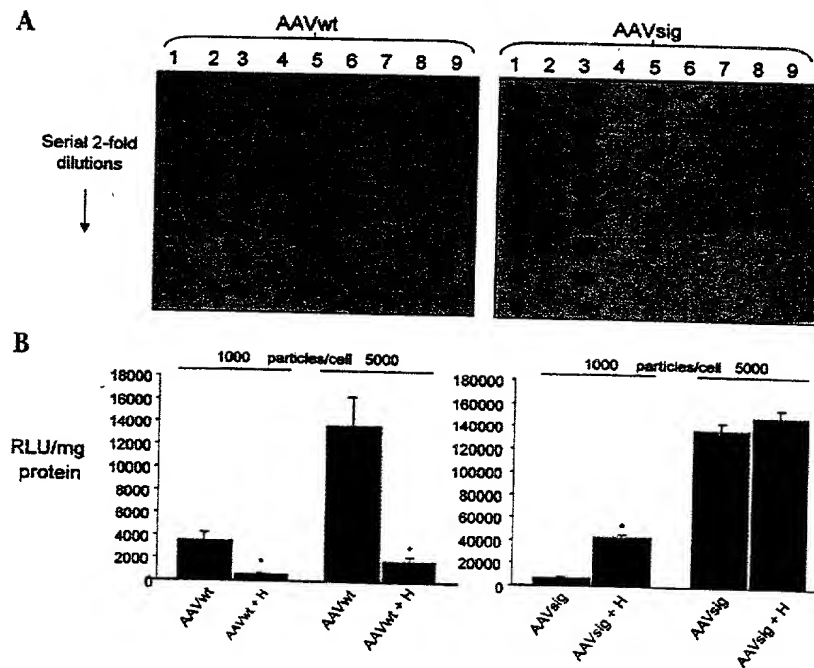
FIGURE 8**FIGURE 9**

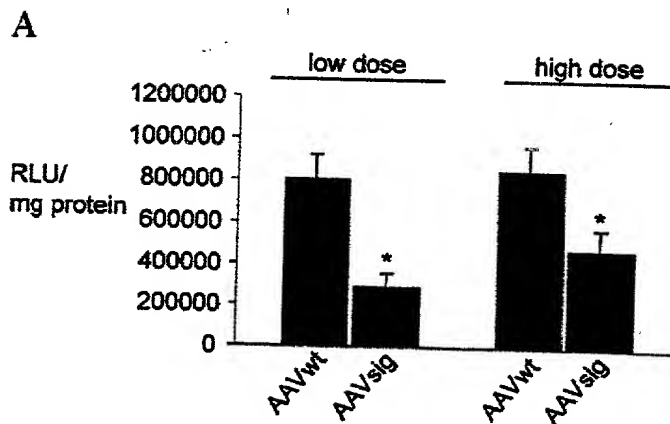
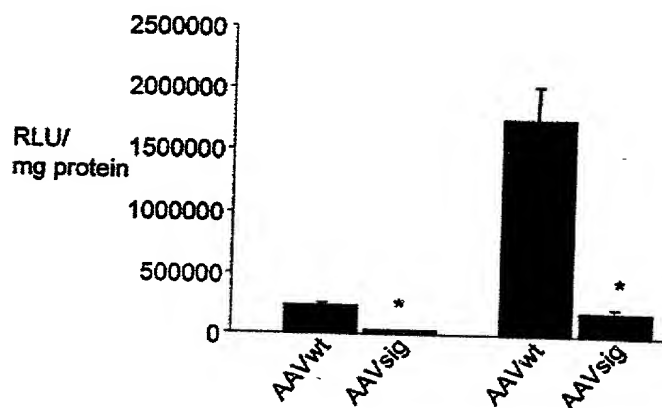
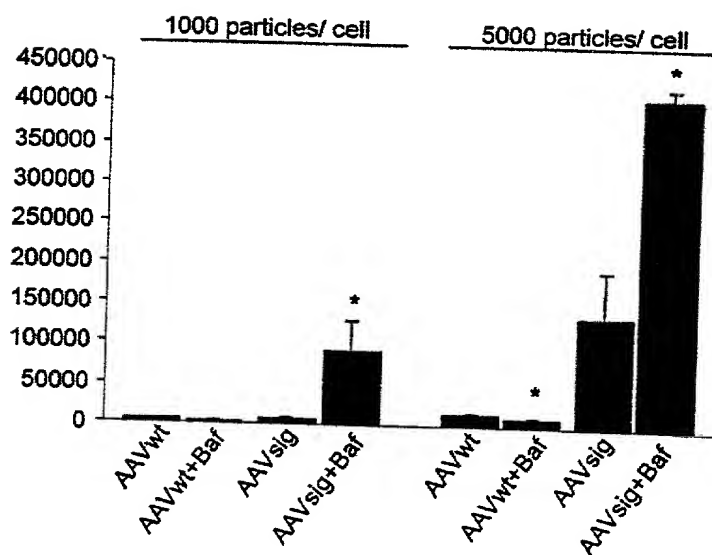
FIGURE 10**B****FIGURE 11**

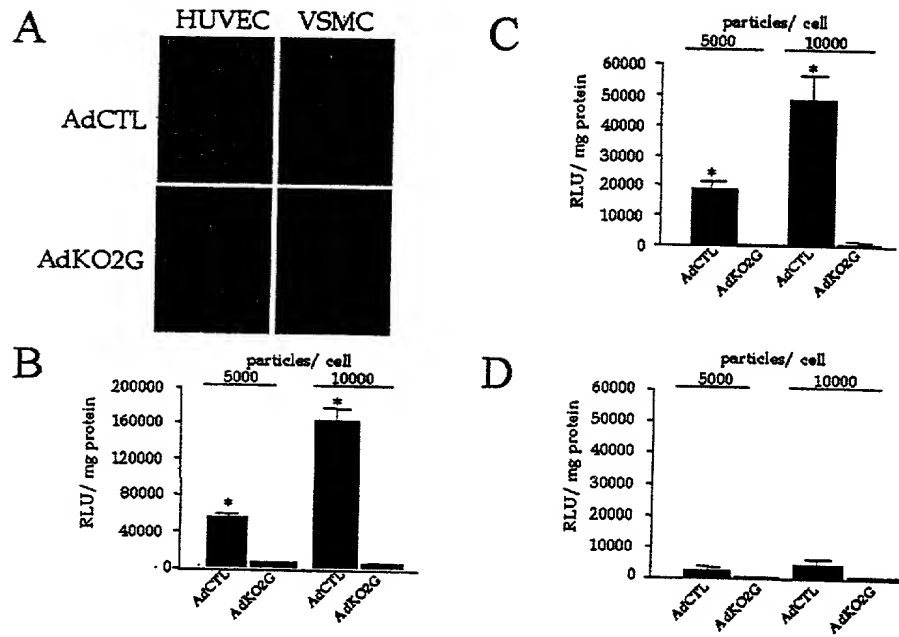
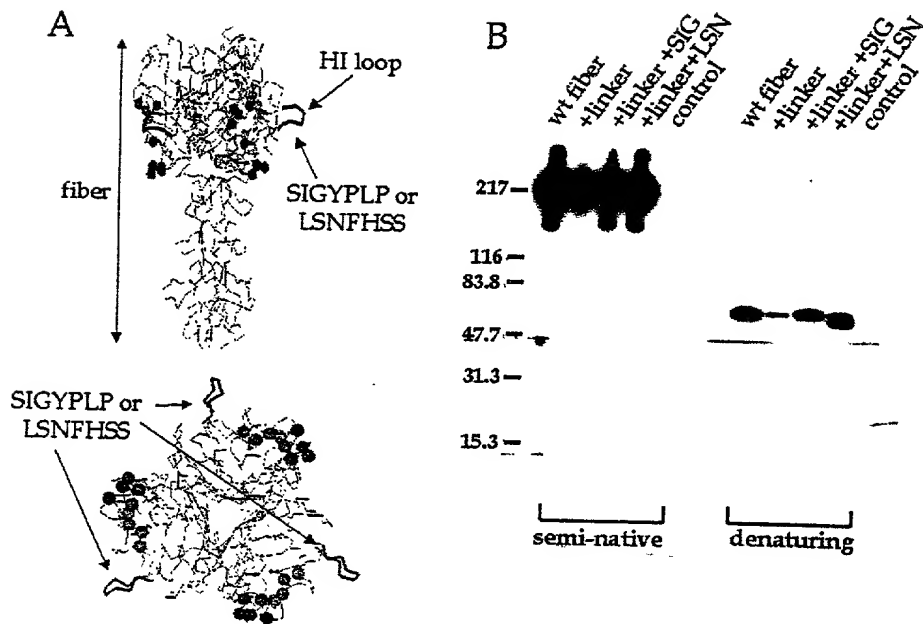
FIGURE 12**FIGURE 13**

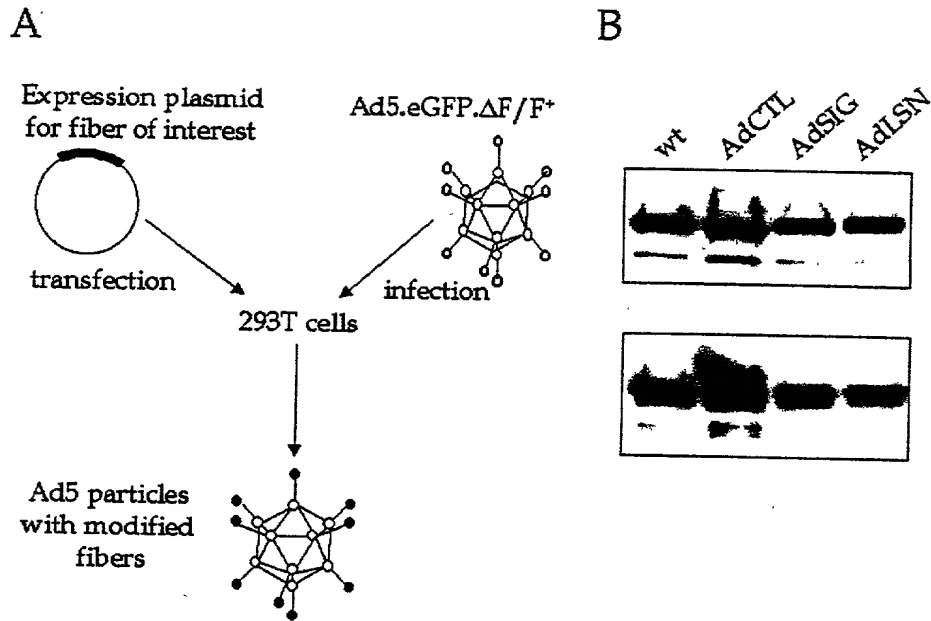
FIGURE 14

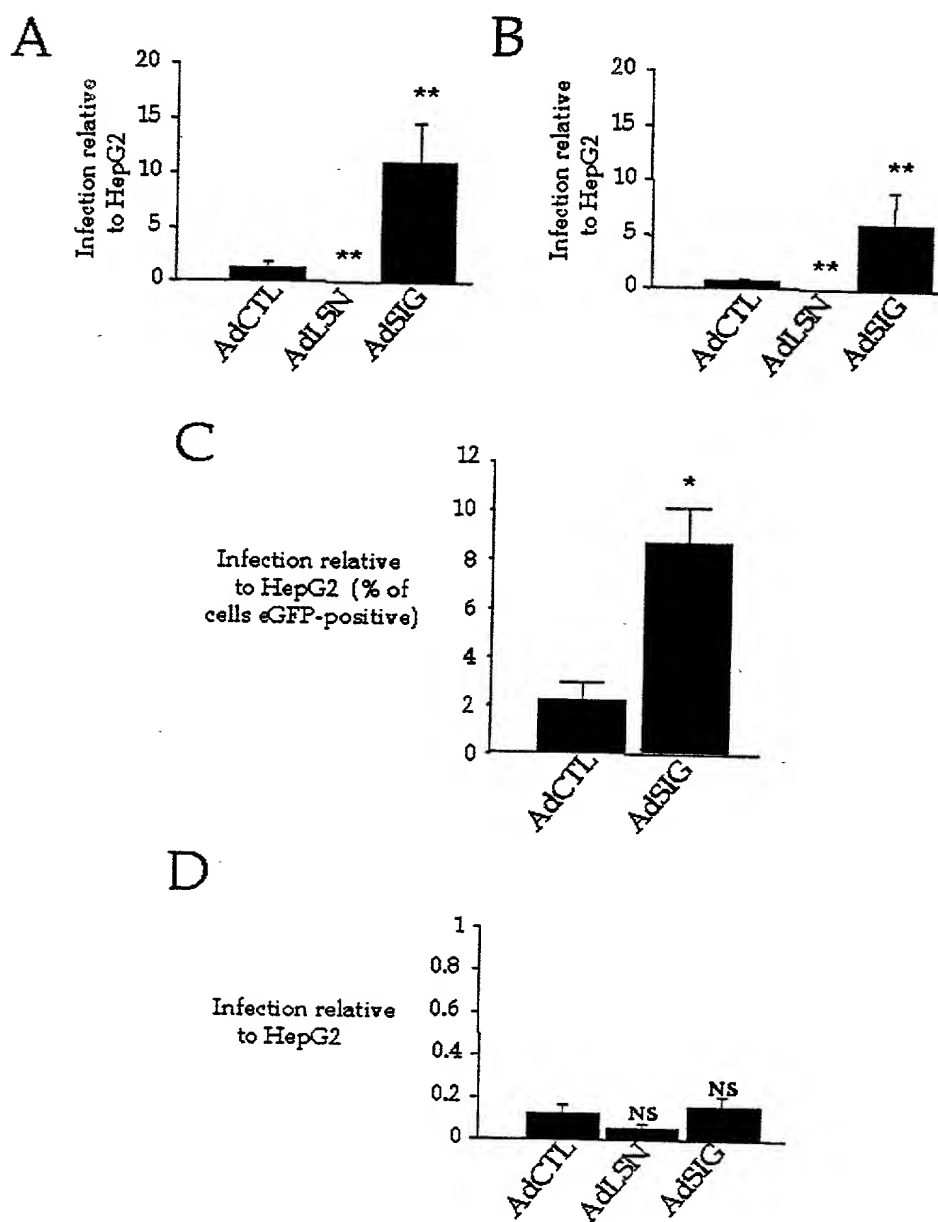
FIGURE 15

FIGURE 16

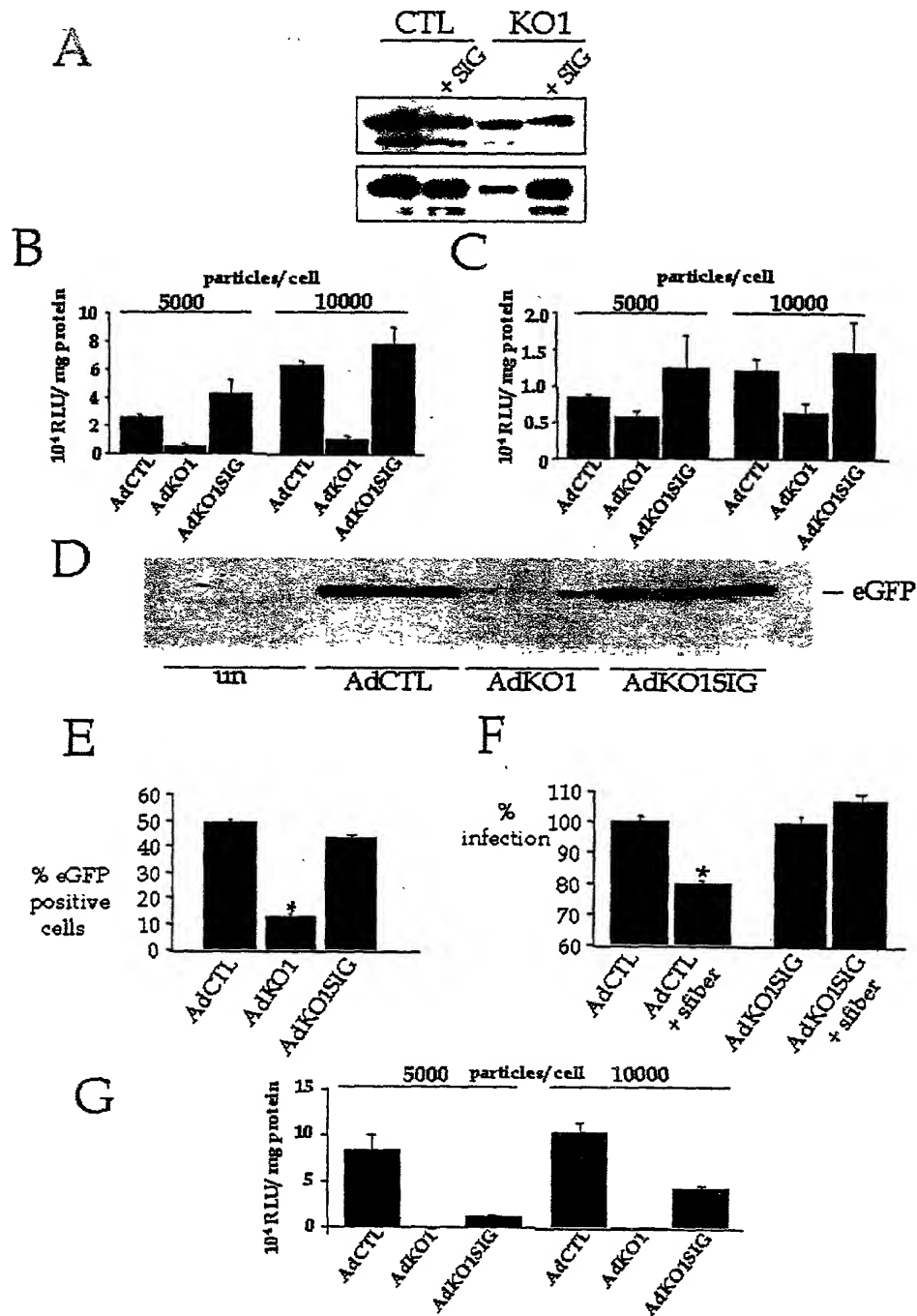
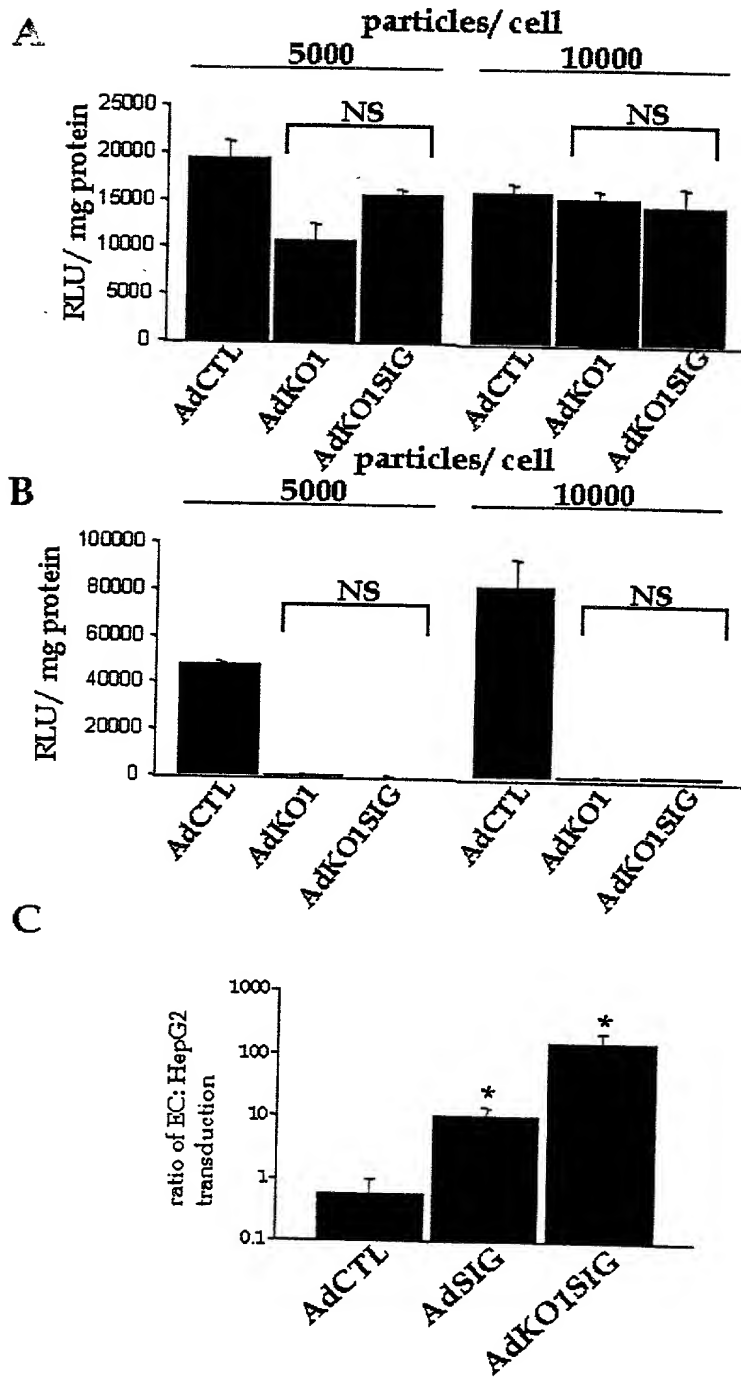


FIGURE 17

12/14

FIGURE 18

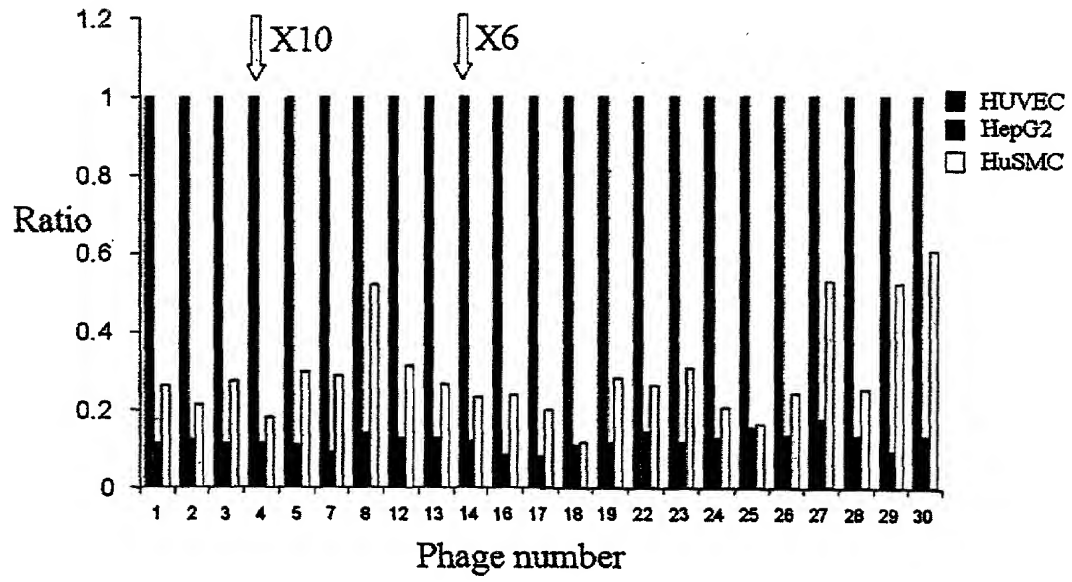


FIGURE 19

1 5	----MSNNPIRPPTS G-	12	39 25	----LSTPLPYDMRR S-	12
2 10	----MSNNPIRPPTS G-	12	40 4	--MSLTTPPAVARP- --	12
3 27	----MSTPPIREQAA H-	12			
4 22	----MSQTPYARPQY V-	12	41 6	--MSLTTPPAVARP- --	12
			42 9	--MSLTTPPAVARP- --	12
5 53	---MSSPTVSSAPQY --	12	43 11	--MSLTTPPAVARP- --	12
6 39	---LQPPSMITHPST --	12	44 15	--MSLTTPPAVARP- --	12
7 43	---LQPPSMITHPST --	12			
8 1	--MAMPQPADHNNS- --	12	45 33	--MSLTTPPAVARP- --	12
			46 34	--MSLTTPPAVARP- --	12
9 45	--MLMPQPAHHNNS- --	12	47 41	--MSLTTPPAVARP- --	12
10 67	--MGMTVPENLIVQ- --	12	48 47	--MSLTTPPAVARP- --	12
11 68	--MGMTVPENLIVQ- --	12			
12 2	-VSGMSVPVQLAR-- --	12	49 48	--MSLTTPPAVARP- --	12
			50 42	----LTPPNQVLNPL Y-	12
13 3	---MTQTPR-TTPWP D-	12	51 29	---MTPIATSIPPQM --	12
14 28	---MTNLPT-VTQFP P-	12	52 35	---MTQQPPLPHPAK --	12
15 23	---MTSNPH-LNPGP R-	12			
16 52	--SMRGLPE-LNPRI --	12	53 58	---MAINDTYPPPRP --	12
			54 32	----MTSPHPQTPNL T-	12
17 63	LTSPFSTP--LNPR- --	12	55 54	---VLSMQTPPTPLL --	12
18 70	LTSPFSTP--LNPR- --	12	56 30	--MTPTTPIPSLPQ- --	12
19 8	---MTGSQQT LHPPP --	12			
20 61	---MQRPQT LTPAS --	12	57 24	--MGHNINIPRTPL- --	12
			58 60	---LAQNPIYRAHPH --	12
21 26	---MTRIQDSPYDLR --	12	59 62	----LTVVPVVSFAV H-	12
22 69	---MTPIQSTQYPHS --	12	60 66	----ANTPPHTILST E-	12
23 13	---MNMTPPPHSPPK --	12			
24 16	--AMSMTTMPHSPN- --	12	61 17	---MSDLLIEYPPYI --	12
			62 18	----MTLPHEL RDGA L-	12
25 14	-----MTPFPTSNEA NL	12	63 36	----LAKPLPTTSNT G-	12
26 20	-----MTPFPTSNEA NL	12	64 37	----LSKPIPHIPSS IG	13
27 31	-----MTPFPTSNEA NL	12			
28 40	-----MTPFPTSNEA NL	12	65 49	---SSRIPGFPDPLH --	12
			66 38	---CICRGVGCCLLL --	12
29 51	-----MTPFPTSNEA NL	12	67 44	----AFPMVGGPDH FR	12
30 57	-----MTPFPTSNEA NL	12	68 46	---AQAMANPLGSHI --	12
31 21	-----NPEPTIDE- --	8			
32 64	-----NPEPTIDE- --	8	69 55	----THAMSHLDKAH --	11
			70 50	-----	0
33 7	-MTQVYTTPPTST-- --	12			
34 59	-----MMPPPTSLPS PS	12			
35 12	---MATQPLSGSRLS G-	13			
36 65	---MAGQPKDSSKTL --	12			
37 56	---MAVQPPNTSTSN --	12			
38 19	----AAVPPPYVMSR P-	12			

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---MAGQPKDSSKTL--
---MQPRPQTLTPAS--
---MTNLPT-VTQFPP-
---MSSPTVSSAPQY-
----LTPPNQVLNPLY-
---MTPIATSIPPQM--
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----ANTPPHTILSTE-
---MSDLLIEYPPI-
---MTLPHEL RDGAL-
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---CICRGVGCCLLL--
----AFPMVGGPDPHFR
---AQAMANPLGSHI--
----THAMSHLDKAH--

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